Amendments to the Claims

The current status of the claims is as follows:

Claims 1-163 (Canceled)

164. (New) A set of amplification oligonucleotides comprising:

a first amplification oligonucleotide having a first target binding region that hybridizes to a first target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under amplification conditions, wherein said first amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

a second amplification oligonucleotide having a second target binding region that hybridizes to a second target sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65 under said amplification conditions, wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase,

wherein the first and second amplification oligonucleotides are capable of amplifying a target nucleic acid sequence present in a target nucleic acid derived from *Cryptosporidium parvum* under said amplification conditions.

165. (New) The set of amplification oligonucleotides of claim 164, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

166. (New) The set of amplification oligonucleotides of claim 164, wherein:

said first target binding region is from 18 to 35 bases in length and said first amplification oligonucleotide does not include a region in addition to said first target binding region that hybridizes to said target nucleic acid or its complement under said amplification conditions; and

said second target binding region is from 18 to 35 bases in length and said second amplification oligonucleotide does not include a region in addition to said second target binding region that hybridizes to said target nucleic acid or its complement under said amplification conditions.

167. (New) The set of amplification oligonucleotides of claim 166, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

168. (New) The set of amplification oligonucleotides of claim 164, wherein:

said first amplification oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64; and

said second amplification oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65.

169. (New) The set of amplification oligonucleotides of claim 168, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

170. (New) The set of amplification oligonucleotides of claim 168, wherein:

said first target binding region is up to 35 bases in length and said first amplification oligonucleotide does not include a region in addition to said first target binding region that hybridizes to said target nucleic acid or its complement under said amplification conditions; and

said second target binding region is up to 35 bases in length and said second amplification oligonucleotide does not include a region in addition to said second target binding region that hybridizes to said target nucleic acid or its complement under said amplification conditions.

171. (New) The set of amplification oligonucleotides of claim 170, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

172. (New) The set of amplification oligonucleotides of claim 164, wherein:

the base sequence of said first amplification oligonucleotide consists essentially of a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

the base sequence of said second amplification oligonucleotide consists essentially of a base sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

173. (New) The set of amplification oligonucleotides of claim 172, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

174. (New) The set of amplification oligonucleotides of claim 164, wherein:

the base sequence of said first amplification oligonucleotide consists of or is contained within a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

the base sequence of said second amplification oligonucleotide consists of or is contained within a base sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

175. (New) The set of amplification oligonucleotides of claim 174, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

176. (New) The set of amplification oligonucleotides of claim 174, wherein each of said first and second amplification oligonucleotides is at least 18 bases in length.

177. (New) The set of amplification oligonucleotides of claim 176, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

178. (New) The set of amplification oligonucleotides of claim 164, wherein:

the base sequence of said first amplification oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

the base sequence of said second amplification oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

179. (New) The set of amplification oligonucleotides of claim 178, wherein at least one of said amplification oligonucleotides includes said 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

180. (New) A method for amplifying *Cryptosporidium parvum* nucleic acid that may be present in a sample, said method comprising:

contacting said sample with said first and second amplification oligonucleotides of claim 164 under said amplification conditions; and

amplifying, if present, said target nucleic acid sequence.

181. (New) The method of claim 180 further comprising:

contacting said sample with a hybridization assay probe, said probe comprising a third target binding region that hybridizes to a third target sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17 to form a stable probe:target hybrid under stringent conditions, wherein said probe does not hybridize to nucleic acid derived from *Cryptosporidium*

muris, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* to form a stable probe:non-target hybrid under said stringent conditions; and

determining whether said probe:target hybrid has formed as an indication of the presence of *Cryptosporidium parvum* in said sample.

182. (New) The method of claim 181, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

183. (New) The method of claim 181, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

184. (New) The method of claim 181 further comprising a detectable label.

185. (New) The method of claim 181, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

186. (New) The method of claim 181, wherein:

said first target binding region is from 18 to 35 bases in length and said first amplification oligonucleotide does not include a region in addition to said first target binding region that hybridizes to said target nucleic acid or its complement under said amplification conditions;

said second target binding region is from 18 to 35 bases in length and said second amplification oligonucleotide does not include a region in addition to said second target binding region that hybridizes to said target nucleic acid or its complement under said amplification conditions; and

said third target binding region is from 18 to 35 bases in length and said probe does not include a region in addition to said third target binding region that hybridizes to said target nucleic acid or its complement under said stringent conditions.

187. (New) The method of claim 186, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

188. (New) The method of claim 186, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

189. (New) The method of claim 186 further comprising a detectable label.

190. (New) The method of claim 186, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

191. (New) A method for amplifying *Cryptosporidium parvum* nucleic acid that may be present in a sample, said method comprising:

contacting said sample with said first and second amplification oligonucleotides of claim 168 under said amplification conditions; and

amplifying, if present, said target nucleic acid sequence.

192. (New) The method of claim 191 further comprising:

contacting said sample with a hybridization assay probe, said probe comprising a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17, wherein said probe forms a stable probe:target hybrid with said target nucleic acid or its complement under stringent conditions, and wherein said probe does not form a stable probe:non-target hybrid with nucleic acid derived from *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* under said stringent conditions; and

determining whether said probe:target hybrid has formed as an indication of the presence of *Cryptosporidium parvum* in said sample.

193. (New) The method of claim 192, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

194. (New) The method of claim 192, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

195. (New) The method of claim 192 further comprising a detectable label.

196. (New) The method of claim 192, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

197. (New) The method of claim 192, wherein:

said first target binding region is up to 35 bases in length and said first amplification oligonucleotide does not include a region in addition to said first target binding region that hybridizes to said target nucleic acid or its complement under said amplification conditions;

said second target binding region is up to 35 bases in length and said second amplification oligonucleotide does not include a region in addition to said second target binding region that hybridizes to said target nucleic acid or its complement under said amplification conditions; and

said probe is up to 35 bases in length.

198. (New) The method of claim 197, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

199. (New) The method of claim 197, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

200. (New) The method of claim 197 further comprising a detectable label.

201. (New) The method of claim 197, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

202. (New) A method for amplifying *Cryptosporidium parvum* nucleic acid that may be present in a sample, said method comprising:

contacting said sample with said first and second amplification oligonucleotides of claim 172 under said amplification conditions; and

amplifying, if present, said target nucleic acid sequence.

203. (New) The method of claim 202 further comprising:

contacting said sample with a hybridization assay probe, said probe comprising a third target binding region, wherein the base sequence of said third target binding region consists essentially of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17, wherein said probe forms a stable probe:target hybrid with said target nucleic acid or its complement under stringent conditions, wherein said probe does not include a region in addition to said third target binding region that hybridizes to said target nucleic acid or its complement under said stringent conditions, and wherein said probe does not form a stable probe:non-target hybrid with nucleic acid derived from *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* under said stringent conditions; and

determining whether said probe:target hybrid has formed as an indication of the presence of *Cryptosporidium parvum* in said sample.

204. (New) The method of claim 203, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

205. (New) The method of claim 203, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

206. (New) The method of claim 203 further comprising a detectable label.

207. (New) The method of claim 203, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

208. (New) A method for amplifying *Cryptosporidium parvum* nucleic acid that may be present in a sample, said method comprising:

contacting said sample with said first and second amplification oligonucleotides of claim 174 under said amplification conditions; and

amplifying, if present, said target nucleic acid sequence.

209. (New) The method of claim 208 further comprising:

contacting said sample with a hybridization assay probe, said probe comprising a third target binding region, wherein the base sequence of said third target binding region consists of or is contained within a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17, wherein said probe forms a stable probe:target hybrid with said target nucleic acid or its complement under stringent conditions, wherein said probe does not include a region in addition to said third target binding region that hybridizes to said target nucleic acid or its complement under said stringent conditions, and wherein said probe does not form a stable probe:non-target hybrid with nucleic acid derived from *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* under said stringent conditions; and

determining whether said probe:target hybrid has formed as an indication of the presence of *Cryptosporidium parvum* in said sample.

210. (New) The method of claim 209, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

211. (New) The method of claim 209, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

212. (New) The method of claim 209 further comprising a detectable label.

213. (New) The method of claim 209, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

214. (New) The method of claim 209, wherein each of said first and second amplification oligonucleotides and said probe is at least 18 bases in length.

215. (New) The method of claim 214, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

216. (New) The method of claim 214, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

217. (New) The method of claim 214 further comprising a detectable label.

218. (New) The method of claim 214, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

219. (New) A method for amplifying *Cryptosporidium parvum* nucleic acid that may be present in a sample, said method comprising:

contacting said sample with said amplification oligonucleotides of claim 178 under said amplification conditions; and

amplifying, if present, said target nucleic acid sequence.

220. (New) The method of claim 219 further comprising:

contacting said sample with a hybridization assay probe, said probe comprising a third target binding region, wherein the base sequence of said third target binding region consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17, wherein said probe forms a stable probe:target hybrid with said target nucleic acid or its complement under stringent conditions, wherein said probe does not include a region in addition to said third target binding region that hybridizes to said target nucleic acid or its complement under said stringent conditions, and wherein said probe does not form a stable probe:non-target hybrid with nucleic acid derived from *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* under said stringent conditions; and

determining whether said probe:target hybrid has formed as an indication of the presence of *Cryptosporidium parvum* in said sample.

221. (New) The method of claim 220, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

222. (New) The method of claim 220, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

223. (New) The method of claim 220 further comprising a detectable label.

224. (New) The method of claim 220, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

225. (New) A kit for use in detecting the presence of *Cryptosporidium parvum* in a sample, said kit comprising:

a first amplification oligonucleotide having a first target binding region that hybridizes to a first target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under amplification conditions, wherein said first amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase;

a second amplification oligonucleotide having a second target binding region that hybridizes to a second target sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ

ID NO:59 and SEQ ID NO:65 under said amplification conditions, wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase,

wherein the first and second amplification oligonucleotides are capable of amplifying a target nucleic acid sequence present in a target nucleic acid derived from *Cryptosporidium parvum* under said amplification conditions; and

a hybridization assay probe, said probe comprising a third target binding region that hybridizes to a third target sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17 to form a stable probe:target hybrid under stringent conditions, wherein said third target sequence is present in said target nucleic acid sequence or its complement, and wherein said probe does not hybridize to nucleic acid derived from *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* to form a stable probe:non-target hybrid under said stringent conditions.

226. (New) The kit of claim 225, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

227. (New) The kit of claim 225, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

228. (New) The kit of claim 225 further comprising a detectable label.

229. (New) The kit of claim 225, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

230. (New) The kit of claim 225, wherein:

said first target binding region is from 18 to 35 bases in length and said first amplification oligonucleotide does not include a region in addition to said first target binding that hybridizes to said target nucleic acid under said amplification conditions;

said second target binding region is from 18 to 35 bases in length and said second amplification oligonucleotide does not include a region in addition to said second target binding that hybridizes to said target nucleic acid under said amplification conditions; and

said probe is from 18 to 35 bases in length.

231. (New) The kit of claim 230, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

232. (New) The kit of claim 230, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

233. (New) The kit of claim 230 further comprising a detectable label.

234. (New) The kit of claim 230, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

235. (New) The kit of claim 225, wherein:

said first amplification oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64;

said second amplification oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65; and

said probe comprises a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17.

236. (New) The kit of claim 235, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

237. (New) The kit of claim 235, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

238. (New) The kit of claim 235 further comprising a detectable label.

239. (New) The kit of claim 235, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

240. (New) The kit of claim 235, wherein:

said first target binding region is up to 35 bases in length and said first amplification oligonucleotide does not include a base region in addition to said first target binding that hybridizes to said target nucleic acid under said amplification conditions;

said second target binding region is up to 35 bases in length and said second amplification oligonucleotide does not include a base region in addition to said second target binding that hybridizes to said target nucleic acid under said amplification conditions; and

said probe is up to 35 bases in length.

241. (New) The kit of claim 240, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

242. (New) The kit of claim 240, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

243. (New) The kit of claim 240 further comprising a detectable label.

244. (New) The kit of claim 240, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

245. (New) The kit of claim 225, wherein:

the base sequence of said first amplification oligonucleotide consists essentially of a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase;

the base sequence of said second amplification oligonucleotide consists essentially of a base sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and

SEQ ID NO:65 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

the base sequence of said third target binding region consists essentially of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17.

246. (New) The kit of claim 245, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

247. (New) The kit of claim 245, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

248. (New) The kit of claim 245 further comprising a detectable label.

249. (New) The kit of claim 245, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

250. (New) The kit of claim 225, wherein:

the base sequence of said first amplification oligonucleotide consists of or is contained within a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase;

the base sequence of said second amplification oligonucleotide consists of or is contained within a base sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID

NO:59 and SEQ ID NO:65 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

the base sequence of said third target binding region consists of or contained within a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17, wherein said probe does not include a region in addition to said third target binding region that hybridizes to said target nucleic acid or its complement under said stringent conditions.

251. (New) The kit of claim 250, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

252. (New) The kit of claim 250, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

253. (New) The kit of claim 250 further comprising a detectable label.

254. (New) The kit of claim 250, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

255. (New) The kit of claim 250, wherein each of said first and second amplification oligonucleotides and said probe is at least 18 bases in length.

256. (New) The kit of claim 255, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

257. (New) The kit of claim 255, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

258. (New) The kit of claim 255 further comprising a detectable label.

259. (New) The kit of claim 255, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.

260. (New) The kit of claim 225, wherein:

the base sequence of said first amplification oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase;

the base sequence of said second amplification oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65 and, optionally, a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

the base sequence of said third target binding region consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17, wherein

said probe does not include a region in addition to said third target binding region that hybridizes to said target nucleic acid or its complement under said stringent conditions.

261. (New) The kit of claim 260, wherein at least one of said first and second amplification oligonucleotides includes a 5' sequence that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

262. (New) The kit of claim 260, wherein said probe comprises at least one base region that does not stably hybridize to said target nucleic acid or its complement under said stringent conditions.

263. (New) The kit of claim 260 further comprising a detectable label.

264. (New) The kit of claim 260, wherein said third target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety or a pseudo peptide backbone which joins at least a portion of the bases of said third target binding region.